

## SEQUENCE LISTING

<110> TRANSFERT PLUS

BELIVEAU, Richard

DEMEULE, Michel

BERTRAND, Yanick

MICHAUD-LEVESQUE, Jonathan

ROLLAND, Yanneve

JODOIN, Julie

<120> Compound and Method for Regulating

Plasminogen Activation and Cell Migration

<130> 15656-10PCT

<150> US 60/469,000

<151> 2003-05-09

<160> 19

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 738

<212> PRT

<213> Homo Sapiens

&lt;400&gt; 1

Met Arg Gly Pro Ser Gly Ala Leu Trp Leu Leu Leu Ala Leu Arg Thr

1 5 10 15

Val Leu Gly Gly Met Glu Val Arg Trp Cys Ala Thr Ser Asp Pro Glu

20 25 30

Gln His Lys Cys Gly Asn Met Ser Glu Ala Phe Arg Glu Ala Gly Ile

35 40 45

Gln Pro Ser Leu Leu Cys Val Arg Gly Thr Ser Ala Asp His Cys Val

50 55 60

Gln Leu Ile Ala Ala Gln Glu Ala Asp Ala Ile Thr Leu Asp Gly Gly

65 70 75 80

Ala Ile Tyr Glu Ala Gly Lys Glu His Gly Leu Lys Pro Val Val Gly

85 90 95

Glu Val Tyr Asp Gln Glu Val Gly Thr Ser Tyr Tyr Ala Val Ala Val

100 105 110

Val Arg Arg Ser Ser His Val Thr Ile Asp Thr Leu Lys Gly Val Lys

115 120 125

Ser Cys His Thr Gly Ile Asn Arg Thr Val Gly Trp Asn Val Pro Val

130 135 140

Gly Tyr Leu Val Glu Ser Gly Arg Leu Ser Val Met Gly Cys Asp Val

145 150 155 160

Leu Lys Ala Val Ser Asp Tyr Phe Gly Gly Ser Cys Val Pro Gly Ala

165 170 175

Gly Glu Thr Ser Tyr Ser Glu Ser Leu Cys Arg Leu Cys Arg Gly Asp

180 185 190

Ser Ser Gly Glu Gly Val Cys Asp Lys Ser Pro Leu Glu Arg Tyr Tyr

195 200 205

Asp Tyr Ser Gly Ala Phe Arg Cys Leu Ala Glu Gly Ala Gly Asp Val  
210 215 220

Ala Phe Val Lys His Ser Thr Val Leu Glu Asn Thr Asp Gly Lys Thr  
225 230 235 240

Leu Pro Ser Trp Gly Gln Ala Leu Leu Ser Gln Asp Phe Glu Leu Leu  
245 250 255

Cys Arg Asp Gly Ser Arg Ala Asp Val Thr Glu Trp Arg Gln Cys His  
260 265 270

Leu Ala Arg Val Pro Ala His Ala Val Val Val Arg Ala Asp Thr Asp  
275 280 285

Gly Gly Leu Ile Phe Arg Leu Leu Asn Glu Gly Gln Arg Leu Phe Ser  
290 295 300

His Glu Gly Ser Ser Phe Gln Met Phe Ser Ser Glu Ala Tyr Gly Gln  
305 310 315 320

Lys Asp Leu Leu Phe Lys Asp Ser Thr Ser Glu Leu Val Pro Ile Ala  
325 330 335

Thr Gln Thr Tyr Glu Ala Trp Leu Gly His Glu Tyr Leu His Ala Met  
340 345 350

Lys Gly Leu Leu Cys Asp Pro Asn Arg Leu Pro Pro Tyr Leu Arg Trp  
355 360 365

Cys Val Leu Ser Thr Pro Glu Ile Gln Lys Cys Gly Asp Met Ala Val  
370 375 380

Ala Phe Arg Arg Gln Arg Leu Lys Pro Glu Ile Gln Cys Val Ser Ala  
385 390 395 400

Lys Ser Pro Gln His Cys Met Glu Arg Ile Gln Ala Glu Gln Val Asp  
405 410 415

Ala Val Thr Leu Ser Gly Glu Asp Ile Tyr Thr Ala Gly Lys Lys Tyr  
420 425 430

Gly Leu Val Pro Ala Ala Gly Glu His Tyr Ala Pro Glu Asp Ser Ser  
435 440 445

Asn Ser Tyr Tyr Val Val Ala Val Val Arg Arg Asp Ser Ser His Ala  
450 455 460

Phe Thr Leu Asp Glu Leu Arg Gly Lys Arg Ser Cys His Ala Gly Phe  
465 470 475 480

Gly Ser Pro Ala Gly Trp Asp Val Pro Val Gly Ala Leu Ile Gln Arg  
485 490 495

Gly Phe Ile Arg Pro Lys Asp Cys Asp Val Leu Thr Ala Val Ser Glu  
500 505 510

Phe Phe Asn Ala Ser Cys Val Pro Val Asn Asn Pro Lys Asn Tyr Pro  
515 520 525

Ser Ser Leu Cys Ala Leu Cys Val Gly Asp Glu Gln Gly Arg Asn Lys  
530 535 540

Cys Val Gly Asn Ser Gln Glu Arg Tyr Tyr Gly Tyr Arg Gly Ala Phe  
545 550 555 560

Arg Cys Leu Val Glu Asn Ala Gly Asp Val Ala Phe Val Arg His Thr  
565 570 575

Thr Val Phe Asp Asn Thr Asn Gly His Asn Ser Glu Pro Trp Ala Ala  
580 585 590

Glu Leu Arg Ser Glu Asp Tyr Glu Leu Leu Cys Pro Asn Gly Ala Arg  
595 600 605

Ala Glu Val Ser Gln Phe Ala Ala Cys Asn Leu Ala Gln Ile Pro Pro  
610 615 620

His Ala Val Met Val Arg Pro Asp Thr Asn Ile Phe Thr Val Tyr Gly  
625 630 635 640

Leu Leu Asp Lys Ala Gln Asp Leu Phe Gly Asp Asp His Asn Lys Asn  
645 650 655

Gly Phe Lys Met Phe Asp Ser Ser Asn Tyr His Gly Gln Asp Leu Leu  
660 665 670  
Phe Lys Asp Ala Thr Val Arg Ala Val Pro Val Gly Glu Lys Thr Thr  
675 680 685  
Tyr Arg Gly Trp Leu Gly Leu Asp Tyr Val Ala Ala Leu Glu Gly Met  
690 695 700  
Ser Ser Gln Gln Cys Ser Gly Ala Ala Ala Pro Ala Pro Gly Ala Pro  
705 710 715 720  
Leu Leu Pro Leu Leu Leu Pro Ala Leu Ala Ala Arg Leu Leu Pro Pro  
725 730 735  
Ala Leu

<210> 2

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer sequence

<400> 2

agaagttagca ggaccagagg g

21

<210> 3

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense primer sequence

<400> 3

tcagtaccca ggcagttatg c

21

<210> 4

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> primer sequence

<400> 4

tctctccctt ctccaaagac cc

22

<210> 5

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense primer sequence

<400> 5

tcaatgagtc cagccagtc gc

22

<210> 6

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> primer sequence

<400> 6

cggagcagtg tggcttattt tc

22

<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense primer sequence

<400> 7

caggtgtatt gggtgtcaag gc

22

<210> 8

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> primer sequence

<400> 8

ggacccaaca agttcaagtg tcac

24

<210> 9

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense primer sequence

<400> 9

aagaagaggt aggcgatgga gc

22

<210> 10

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> primer sequence

<400> 10

ccttgaagat gatggactac cctcg

25

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense primer sequence

<400> 11

aaaacccaaa aaagccccc cagc

24

<210> 12

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> primer sequence

<400> 12

accgagggttg tgggtgggtt agac

24

<210> 13

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense primer sequence

<400> 13

caggaagtgg aagggtgtcgt tg

22

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer sequence

<400> 14

ccatcaccat cttccaggag

20

<210> 15

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense primer sequence

<400> 15

cctgcttcac caccttcttg

20

<210> 16

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> primer sequence

<400> 16

aaagacattg cgtggtcagg cagc

24

<210> 17

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense primer sequence

<400> 17

ggcatcataa ggcagtcgtt cac

23

<210> 18

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> primer sequence

<400> 18

ccagcacata ggagagatga gctt

24

<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense primer sequence

<400> 19

ggtgtggtgg tgacatggtt aatc

24